

PRELIMINARY AMENDMENT

In the specification:

Please amend page 10, lines 11 to 27, to recite as follows:

Figure 3 shows the results of one embodiment of the method of this invention that utilizes tBLAST alignment for the identification of a "favorable reaction type" iECTA. Shown in the figure is a tBLAST alignment of *Pseudomonas aeruginosa* acetolactate synthase large subunit amino acid sequence (Seq. ID Nos. 1, 4 and 7) with the human expressed sequence tag database (translated in all six possible reading frames) (Seq. ID Nos. 3, 6 and 9). The low "Expect" (E) values indicate that it is extremely unlikely that any of these alignments could occur by chance alone. Only the ten best E values and the best alignment are shown (Seq. ID Nos. 2, 5 and 8).

Figure 4 shows the results of one embodiment of the method of this invention that utilizes tBLAST alignment for the identification of a "favorable reaction type" iECTA. Shown in the figure is a tBLAST alignment of *Pseudomonas aeruginosa* acetolactate synthase small subunit amino acid sequence (Seq. ID No. 10) with the human expressed sequence tag database (translated in all six possible reading frames) (Seq. ID No. 12). E values = 6.5 indicating that the alignment shown (Seq. ID No. 11) would be predicted to be found more than six times in the expresses tag database due to chance alone.

A marked up version of page 10, lines 11 to 27, is attached for the Office's convenience.

Applicants also respectfully request that the attached paper copy of the sequences identified above be amended into the subject application papers. An issue of new matter is not raised by these amendments. Support is found on page 10 and Figures 3 and 4 as originally filed. Entry of these amendments is respectfully requested.

In the unlikely event that the transmittal letter is separated from this document and/or the Patent Office determines that an extension and/or other relief is required, Applicants petition for any required relief including extensions of time and authorize the Commissioner to

charge the cost of such petitions and/or other fees due in connection with the filing of this document to **Deposit Account No. 50-1189**, referencing billing reference **23896-7101**. However, the Commissioner is not authorized to charge the cost of the issue fee to the Deposit Account.

Respectfully submitted,

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MARKED-UP VERSION SHOWING CHANGES MADE TO PAGE 10

Please amend page 10, lines 11 to 27, by addition of the following underlined terms.

Figure 3 shows the results of one embodiment of the method of this invention that utilizes tBLAST alignment for the identification of a "favorable reaction type" iECTA. Shown in the figure is a tBLAST alignment of *Pseudomonas aeruginosa* acetolactate synthase large subunit amino acid sequence (Seq. ID Nos. 1, 4 and 7) with the human expressed sequence tag database (translated in all six possible reading frames) (Seq. ID Nos. 3, 6 and 9). The low "Expect" (E) values indicate that it is extremely unlikely that any of these alignments could occur by chance alone. Only the ten best E values and the best alignment are shown (Seq. ID Nos. 2, 5 and 8).

Figure 4 shows the results of one embodiment of the method of this invention that utilizes tBLAST alignment for the identification of a "favorable reaction type" iECTA. Shown in the figure is a tBLAST alignment of *Pseudomonas aeruginosa* acetolactate synthase small subunit amino acid sequence (Seq. ID No. 10) with the human expressed sequence tag database (translated in all six possible reading frames) (Seq. ID No. 12). E values = 6.5 indicating that the alignment shown (Seq. ID No. 11) would be predicted to be found more than six times in the expresses tag database due to chance alone.